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3/32

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4/32

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Gln Thr Val Tyr Glu Trp Cys Gly Val Val Thr Gln Leu Leu Ser Ala
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Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Gln
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Lys Asp Ile Leu Ile Arg Ile Leu Asp Asp Gly Val Lys Lys Leu Asn
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13/32

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atc gaa acc gca gat ggg gca tta gat ctt tat aac aaa tac ctc gac          96
Ile Glu Thr Ala Asp Gly Ala Leu Asp Leu Tyr Asn Lys Tyr Leu Asp
                20                  25                  30

cag gtc atc ccc tgg aag acc ttt gat gaa acc ata aaa gag tta agc         144
Gln Val Ile Pro Trp Lys Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser
            35                  40                  45

cgt ttt aaa cag gag tac tcg cag gaa gct tct gtt tta gtt ggt gat         192
Arg Phe Lys Gln Glu Tyr Ser Gln Glu Ala Ser Val Leu Val Gly Asp
        50                  55                  60

att aaa gtt ttg ctt atg gac agc cag gac aag tat ttt gaa gcg aca         240
Ile Lys Val Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr
65                  70                  75                  80

caa act gtt tat gaa tgg tgt ggt gtc gtg acg caa tta ctc tca gcg         288
Gln Thr Val Tyr Glu Trp Cys Gly Val Val Thr Gln Leu Leu Ser Ala
                85                  90                  95

tat att tta cta ttt gat gaa tat aat gag aaa aaa gca tca gcc cag         336
Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Gln
            100                 105                 110

aaa gac att ctc att agg ata tta gat gat ggt gtc aag aaa ctg aat         384
Lys Asp Ile Leu Ile Arg Ile Leu Asp Asp Gly Val Lys Lys Leu Asn
        115                 120                 125

gaa gcg caa aaa tct ctc ctg aca agt tca caa agt ttc aac aac gct         432
Glu Ala Gln Lys Ser Leu Leu Thr Ser Ser Gln Ser Phe Asn Asn Ala
    130                 135                 140

tcc gga aaa ctg ctg gca tta gat agc cag tta act aat gat ttt tcg         480
Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr Asn Asp Phe Ser
145                 150                 155                 160

gaa aaa agt agt tat ttc cag tca cag gtg gat aga att cgt aag gaa         528
Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Arg Ile Arg Lys Glu
                165                 170                 175
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gct tat gcc ggt gct gca gcc ggc ata gtc gcc ggt ccg ttt gga tta        576
Ala Tyr Ala Gly Ala Ala Ala Gly Ile Val Ala Gly Pro Phe Gly Leu
            180                 185                 190

att att tcc tat tct att gct gcg ggc gtg att gaa ggg aaa ttg att        624
Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Ile Glu Gly Lys Leu Ile
            195                 200                 205

cca gaa ttg aat aac agg cta aaa aca gtg caa aat ttc ttt act agc        672
Pro Glu Leu Asn Asn Arg Leu Lys Thr Val Gln Asn Phe Phe Thr Ser
    210                 215                 220

tta tca gct aca gtg aaa caa gcg aat aaa gat atc gat gcg gca aaa        720
Leu Ser Ala Thr Val Lys Gln Ala Asn Lys Asp Ile Asp Ala Ala Lys
225                 230                 235                 240

ttg aaa tta gcc act gaa ata gca gca att ggg gag ata aaa acg gaa        768
Leu Lys Leu Ala Thr Glu Ile Ala Ala Ile Gly Glu Ile Lys Thr Glu
                245                 250                 255

acc gaa aca acc aga ttc tac gtt gat tat gat gat tta atg ctt tct        816
Thr Glu Thr Thr Arg Phe Tyr Val Asp Tyr Asp Asp Leu Met Leu Ser
                260                 265                 270

tta tta aaa gga gct gca aag aaa atg att aac acc tgt aat gaa tac        864
Leu Leu Lys Gly Ala Ala Lys Lys Met Ile Asn Thr Cys Asn Glu Tyr
            275                 280                 285

caa caa cgt cat ggt aag aag acg ctt ttc gag gtt cct gac gtc gct        912
Gln Gln Arg His Gly Lys Lys Thr Leu Phe Glu Val Pro Asp Val Ala
    290                 295                 300

agt aaa gaa acg aac caa aag cca tat aag gaa aca tac ggc att tcc        960
Ser Lys Glu Thr Asn Gln Lys Pro Tyr Lys Glu Thr Tyr Gly Ile Ser
305                 310                 315                 320

cat att aca cgc cat gat atg ctg caa atc cct gaa cag caa aaa aat       1008
His Ile Thr Arg His Asp Met Leu Gln Ile Pro Glu Gln Gln Lys Asn
                325                 330                 335

gaa aaa tat caa gtt cct gaa ttc gat tcg tcc aca att aaa aat atc       1056
Glu Lys Tyr Gln Val Pro Glu Phe Asp Ser Ser Thr Ile Lys Asn Ile
            340                 345                 350

tct tct gca aaa ggc ctg gac gtt tgg gac agc tgg cca tta caa aac       1104
Ser Ser Ala Lys Gly Leu Asp Val Trp Asp Ser Trp Pro Leu Gln Asn
            355                 360                 365

gct gac ggc act gtc gca aac tat cac ggc tac cac atc gtc ttt gca       1152
Ala Asp Gly Thr Val Ala Asn Tyr His Gly Tyr His Ile Val Phe Ala
    370                 375                 380

tta gcc gga gat cct aaa aat gcg gat gac aca tcg att tac atg ttc       1200
Leu Ala Gly Asp Pro Lys Asn Ala Asp Asp Thr Ser Ile Tyr Met Phe
385                 390                 395                 400
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tat caa aaa gtc ggc gaa act tct att gac agc tgg aaa aac gct ggc    1248
Tyr Gln Lys Val Gly Glu Thr Ser Ile Asp Ser Trp Lys Asn Ala Gly
            405                 410                 415

cgc gtc ttt aaa gac agc gac aaa ttc gat gca aat gat tct atc cta    1296
Arg Val Phe Lys Asp Ser Asp Lys Phe Asp Ala Asn Asp Ser Ile Leu
            420                 425                 430

aaa gac caa aca caa gaa tgg tca ggt tca gcc aca ttt aca tct gac    1344
Lys Asp Gln Thr Gln Glu Trp Ser Gly Ser Ala Thr Phe Thr Ser Asp
            435                 440                 445

gga aaa atc cgt tta ttc tac act gat ttc tcc ggt aaa cat tac ggc    1392
Gly Lys Ile Arg Leu Phe Tyr Thr Asp Phe Ser Gly Lys His Tyr Gly
        450                 455                 460

aaa caa aca ctg aca act gca caa gtt aac gta tca gca tca gac agc    1440
Lys Gln Thr Leu Thr Thr Ala Gln Val Asn Val Ser Ala Ser Asp Ser
465                 470                 475                 480

tct ttg aac atc aac ggt gta gag gat tat aaa tca atc ttt gac ggt    1488
Ser Leu Asn Ile Asn Gly Val Glu Asp Tyr Lys Ser Ile Phe Asp Gly
                485                 490                 495

gac gga aaa acg tat caa aat gta cag cag ttc atc gat gaa ggc aac    1536
Asp Gly Lys Thr Tyr Gln Asn Val Gln Gln Phe Ile Asp Glu Gly Asn
            500                 505                 510

tac agc tca ggc gac aac cat acg ctg aga gat cct cac tac gta gaa    1584
Tyr Ser Ser Gly Asp Asn His Thr Leu Arg Asp Pro His Tyr Val Glu
            515                 520                 525

gat aaa ggc cac aaa tac tta gta ttt gaa gca aac act gga act gaa    1632
Asp Lys Gly His Lys Tyr Leu Val Phe Glu Ala Asn Thr Gly Thr Glu
            530                 535                 540

gat ggc tac caa ggc gaa gaa tct tta ttt aac aaa gca tac tat ggc    1680
Asp Gly Tyr Gln Gly Glu Glu Ser Leu Phe Asn Lys Ala Tyr Tyr Gly
545                 550                 555                 560

aaa agc aca tca ttc ttc cgt caa gaa agt caa aaa ctt ctg caa agc    1728
Lys Ser Thr Ser Phe Phe Arg Gln Glu Ser Gln Lys Leu Leu Gln Ser
                565                 570                 575

gat aaa aaa cgc acg gct gag tta gca aac ggc gct ctc ggt atg att    1776
Asp Lys Lys Arg Thr Ala Glu Leu Ala Asn Gly Ala Leu Gly Met Ile
            580                 585                 590

gag cta aac gat gat tac aca ctg aaa aaa gtg atg aaa ccg ctg att    1824
Glu Leu Asn Asp Asp Tyr Thr Leu Lys Lys Val Met Lys Pro Leu Ile
            595                 600                 605

gca tct aac aca gta aca gat gaa att gaa cgc gcg aac gtc ttt aaa    1872
Ala Ser Asn Thr Val Thr Asp Glu Ile Glu Arg Ala Asn Val Phe Lys
        610                 615                 620
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atg aac ggc aaa tgg tac ctg ttc act gac tcc cgc gga tca aaa atg      1920
Met Asn Gly Lys Trp Tyr Leu Phe Thr Asp Ser Arg Gly Ser Lys Met
625             630             635             640

acg att gac ggc att acg tct aac gat att tac atg ctt ggt tat gtt      1968
Thr Ile Asp Gly Ile Thr Ser Asn Asp Ile Tyr Met Leu Gly Tyr Val
                645             650             655

tct aat tct tta act ggc cca tac aag ccg ctg aac aaa act ggc ctt      2016
Ser Asn Ser Leu Thr Gly Pro Tyr Lys Pro Leu Asn Lys Thr Gly Leu
                660             665             670

gtg tta aaa atg gat ctt gat cct aac gat gta acc ttt act tac tca      2064
Val Leu Lys Met Asp Leu Asp Pro Asn Asp Val Thr Phe Thr Tyr Ser
            675             680             685

cac ttc gct gta cct caa gcg aaa gga aac aat gtc gtg att aca agc      2112
His Phe Ala Val Pro Gln Ala Lys Gly Asn Asn Val Val Ile Thr Ser
    690             695             700

tat atg aca aac aga gga ttc tac gca gac aaa caa tca acg ttt gcg      2160
Tyr Met Thr Asn Arg Gly Phe Tyr Ala Asp Lys Gln Ser Thr Phe Ala
705             710             715             720

cca agc ttc ctg ctg aac atc aaa ggc aag aaa aca tct gtt gtc aaa      2208
Pro Ser Phe Leu Leu Asn Ile Lys Gly Lys Lys Thr Ser Val Val Lys
                725             730             735

gac agc atc ctt gaa caa gga caa tta aca gtt aac aaa tag tga          2253
Asp Ser Ile Leu Glu Gln Gly Gln Leu Thr Val Asn Lys
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Gln Val Ile Pro Trp Lys Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser
        35              40              45


Arg Phe Lys Gln Glu Tyr Ser Gln Glu Ala Ser Val Leu Val Gly Asp
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Ile Lys Val Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr
65   70   75   80

Gln Thr Val Tyr Glu Trp Cys Gly Val Val Thr Gln Leu Leu Ser Ala
                85   90   95

Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Gln
            100   105   110

Lys Asp Ile Leu Ile Arg Ile Leu Asp Asp Gly Val Lys Lys Leu Asn
            115   120   125

Glu Ala Gln Lys Ser Leu Leu Thr Ser Ser Gln Ser Phe Asn Asn Ala
    130   135   140

Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr Asn Asp Phe Ser
145   150   155   160

Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Arg Ile Arg Lys Glu
            165   170   175

Ala Tyr Ala Gly Ala Ala Ala Gly Ile Val Ala Gly Pro Phe Gly Leu
            180   185   190

Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Ile Glu Gly Lys Leu Ile
            195   200   205

Pro Glu Leu Asn Asn Arg Leu Lys Thr Val Gln Asn Phe Phe Thr Ser
    210   215   220

Leu Ser Ala Thr Val Lys Gln Ala Asn Lys Asp Ile Asp Ala Ala Lys
225   230   235   240

Leu Lys Leu Ala Thr Glu Ile Ala Ala Ile Gly Glu Ile Lys Thr Glu
            245   250   255

Thr Glu Thr Thr Arg Phe Tyr Val Asp Tyr Asp Asp Leu Met Leu Ser
            260   265   270

Leu Leu Lys Gly Ala Ala Lys Lys Met Ile Asn Thr Cys Asn Glu Tyr

Gln Gln Arg His Gly Lys Lys Thr Leu Phe Glu Val Pro Asp Val Ala
    290   295   300

Ser Lys Glu Thr Asn Gln Lys Pro Tyr Lys Glu Thr Tyr Gly Ile Ser
305   310   315   320

His Ile Thr Arg His Asp Met Leu Gln Ile Pro Glu Gln Gln Lys Asn
                325   330   335

Glu Lys Tyr Gln Val Pro Glu Phe Asp Ser Ser Thr Ile Lys Asn Ile
            340   345   350

Ser Ser Ala Lys Gly Leu Asp Val Trp Asp Ser Trp Pro Leu Gln Asn
    355   360   365

Ala Asp Gly Thr Val Ala Asn Tyr His Gly Tyr His Ile Val Phe Ala
    370   375   380

Leu Ala Gly Asp Pro Lys Asn Ala Asp Asp Thr Ser Ile Tyr Met Phe
385   390   395   400

Tyr Gln Lys Val Gly Glu Thr Ser Ile Asp Ser Trp Lys Asn Ala Gly
            405   410   415

Arg Val Phe Lys Asp Ser Asp Lys Phe Asp Ala Asn Asp Ser Ile Leu
            420   425   430

Lys Asp Gln Thr Gln Glu Trp Ser Gly Ser Ala Thr Phe Thr Ser Asp
            435   440   445

Gly Lys Ile Arg Leu Phe Tyr Thr Asp Phe Ser Gly Lys His Tyr Gly
    450   455   460

Lys Gln Thr Leu Thr Thr Ala Gln Val Asn Val Ser Ala Ser Asp Ser
465   470   475   480

Ser Leu Asn Ile Asn Gly Val Glu Asp Tyr Lys Ser Ile Phe Asp Gly
            485   490   495

Asp Gly Lys Thr Tyr Gln Asn Val Gln Gln Phe Ile Asp Glu Gly Asn

Tyr Ser Ser Gly Asp Asn His Thr Leu Arg Asp Pro His Tyr Val Glu
        515   520   525

Asp Lys Gly His Lys Tyr Leu Val Phe Glu Ala Asn Thr Gly Thr Glu
        530   535   540

Asp Gly Tyr Gln Gly Glu Glu Ser Leu Phe Asn Lys Ala Tyr Tyr Gly
545   550   555   560

Lys Ser Thr Ser Phe Phe Arg Gln Glu Ser Gln Lys Leu Leu Gln Ser
                565   570   575

Asp Lys Lys Arg Thr Ala Glu Leu Ala Asn Gly Ala Leu Gly Met Ile
            580   585   590

Glu Leu Asn Asp Asp Tyr Thr Leu Lys Lys Val Met Lys Pro Leu Ile
        595   600   605

Ala Ser Asn Thr Val Thr Asp Glu Ile Glu Arg Ala Asn Val Phe Lys
        610   615   620

Met Asn Gly Lys Trp Tyr Leu Phe Thr Asp Ser Arg Gly Ser Lys Met
625   630   635   640

Thr Ile Asp Gly Ile Thr Ser Asn Asp Ile Tyr Met Leu Gly Tyr Val
                645   650   655

Ser Asn Ser Leu Thr Gly Pro Tyr Lys Pro Leu Asn Lys Thr Gly Leu
            660   665   670

Val Leu Lys Met Asp Leu Asp Pro Asn Asp Val Thr Phe Thr Tyr Ser
        675   680   685

His Phe Ala Val Pro Gln Ala Lys Gly Asn Asn Val Val Ile Thr Ser
        690   695   700

Tyr Met Thr Asn Arg Gly Phe Tyr Ala Asp Lys Gln Ser Thr Phe Ala
705   710   715   720

Pro Ser Phe Leu Leu Asn Ile Lys Gly Lys Lys Thr Ser Val Val Lys

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        725              730              735

Asp Ser Ile Leu Glu Gln Gly Gln Leu Thr Val Asn Lys
         740                  745


<210>  21
<211>  921
<212>  DNA
<213>  Salmonella typhi

<400>  21
atgactagta ttttgcaga acaaactgta gaggtagtta aaagcgcgat cgaaaccgca      60

gatggggcat tagatcttta taacaaatac ctcgaccagg tcatcccctg gaagaccttt     120

gatgaaacca taaaagagtt aagccgtttt aaacaggagt actcgcagga agcttctgtt     180

ttagttggtg atattaaagt tttgcttatg gacagccagg acaagtattt tgaagcgaca     240

caaactgttt atgaatggtg tggtgtcgtg acgcaattac tctcagcgta tattttacta     300

tttgatgaat ataatgagaa aaaagcatca gcccagaaag acattctcat taggatatta     360

gatgatggtg tcaagaaact gaatgaagcg caaaaatctc tcctgacaag ttcacaaagt     420

ttcaacaacg cttccggaaa actgctggca ttagatagcc agttaactaa tgattttcg       480

gaaaaaagta gttatttcca gtcacaggtg gatagaattc gtaaggaagc ttatgccggt     540

gctgcagccg gcatagtcgc cggtccgttt ggattaatta tttcctattc tattgctgcg     600

ggcgtgattg aagggaaatt gattccagaa ttgaataaca ggctaaaaac agtgcaaaat     660

ttctttacta gcttatcagc tacagtgaaa caagcgaata agatatcga tgcggcaaaa       720

ttgaaattag ccactgaaat agcagcaatt ggggagataa aaacggaaac cgaaacaacc     780

agattctacg ttgattatga tgatttaatg ctttctttat aaaaggagc tgcaaagaaa       840

atgattaaca cctgtaatga ataccaacaa cgtcatggta agaagacgct tttcgaggtt     900

cctgacgtcg ctagctgata a                                                921


<210>  22
<211>  1102
<212>  DNA
<213>  Salmonella typhi

<400>  22
ggaggtaata ggtaagaata ctttataaaa caggtactta attgcaattt atatatttaa       60

agaggcaaat gattatgacc ggaatatttg cagaacaaac tgtagaggta gttaaaagcg     120
```

```
cgatcgaaac cgcagatggg gcattagatc tttataacaa atacctcgac caggtcatcc     180

cctggaagac ctttgatgaa accataaaag agttaagccg ttttaaacag gagtactcgc     240

aggaagcttc tgttttagtt ggtgatatta aagttttgct tatggacagc caggacaagt     300

attttgaagc gacacaaact gtttatgaat ggtgtggtgt cgtgacgcaa ttactctcag     360

cgtatatttt actatttgat gaatataatg agaaaaaagc atcagcccag aaagacattc     420

tcattaggat attagatgat ggtgtcaaga aactgaatga agcgcaaaaa tctctcctga     480

caagttcaca aagtttcaac aacgcttccg gaaaactgct ggcattagat agccagttaa     540

ctaatgattt ttcggaaaaa agtagttatt tccagtcaca ggtggataga attcgtaagg     600

aagcttatgc cggtgctgca gccggcatag tcgccggtcc gtttggatta attatttcct     660

attctattgc tgcgggcgtg attgaaggga aattgattcc agaattgaat aacaggctaa     720

aaacagtgca aaatttcttt actagcttat cagctacagt gaaacaagcg aataaagata     780

tcgatgcggc aaaattgaaa ttagccactg aaatagcagc aattggggag ataaaaacgg     840

aaaccgaaac aaccagattc tacgttgatt atgatgattt aatgctttct ttattaaaag     900

gagctgcaaa gaaaatgatt aacacctgta atgaatacca caaagacac ggtaagaaga      960

cgcttttcga ggttcctgac gtctgataca ttttcattcg atctgtgtac ttttaacgcc    1020

cgatagcgta aagaaaatga gagacggaga aaaagcgata ttcaacagcc cgataaacaa    1080

gagtcgttac cgggctgacg ag                                              1102
```

```
<210>   23
<211>   1102
<212>   DNA
<213>   Salmonella paratyphi


<220>
<221>   CDS
<222>   (75)..(986)

<400>   23
ggaggcaata ggtaggaata agttataaaa caatagctta attgcaattt atatatttaa     60

agaggcaaat gatt atg act gga ata ttt gca gaa caa act gta gag gta     110
              Met Thr Gly Ile Phe Ala Glu Gln Thr Val Glu Val
              1               5                  10

gtt aaa agc gcg atc gaa acc gca gat ggg gca tta gat ttt tat aac     158
Val Lys Ser Ala Ile Glu Thr Ala Asp Gly Ala Leu Asp Phe Tyr Asn
     15                  20                  25
```

```
aaa tac ctc gac cag gtt atc ccc tgg aag acc ttt gat gaa acc ata       206
Lys Tyr Leu Asp Gln Val Ile Pro Trp Lys Thr Phe Asp Glu Thr Ile
    30                  35                  40

aaa gag tta agc cgt ttt aaa cag gag tac tcg cag gaa gct tct gtt       254
Lys Glu Leu Ser Arg Phe Lys Gln Glu Tyr Ser Gln Glu Ala Ser Val
45                  50                  55                  60

tta gtt ggt gat att aaa gtt ttg ctt atg gac agc cag gat aag tat       302
Leu Val Gly Asp Ile Lys Val Leu Leu Met Asp Ser Gln Asp Lys Tyr
                65                  70                  75

ttt gaa gcg aca caa act gtt tat gaa tgg tgt ggt gtc gtg acg caa       350
Phe Glu Ala Thr Gln Thr Val Tyr Glu Trp Cys Gly Val Val Thr Gln
                80                  85                  90

tta ctc tca gcg tat att tta cta ttt gat gaa tat aat gag aaa aaa       398
Leu Leu Ser Ala Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys
                95                  100                 105

gca tca gcg cag aaa gac att ctc atc agg ata tta gat gat ggc gtc       446
Ala Ser Ala Gln Lys Asp Ile Leu Ile Arg Ile Leu Asp Asp Gly Val
        110                 115                 120

aat aaa ctg aat gaa gcg caa aaa tct ctc ctg gga agt tca caa agt       494
Asn Lys Leu Asn Glu Ala Gln Lys Ser Leu Leu Gly Ser Ser Gln Ser
125                 130                 135                 140

ttc aac aac gct tca gga aaa ctg ctg gca tta gat agc cag tta act       542
Phe Asn Asn Ala Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr
                145                 150                 155

aat gat ttc tcg gaa aaa agt agt tat ttc cag tca cag gtg gat aga       590
Asn Asp Phe Ser Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Arg
                160                 165                 170

att cgt aag gaa gct tat gcc ggt gct gca gca ggc ata gtc gcc ggt       638
Ile Arg Lys Glu Ala Tyr Ala Gly Ala Ala Ala Gly Ile Val Ala Gly
        175                 180                 185

ccg ttt gga tta att att tcc tat tct att gct gcg ggc gtg att gaa       686
Pro Phe Gly Leu Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Ile Glu
        190                 195                 200

ggg aaa ttg att cca gaa ttg aat gac agg cta aaa gca gtg caa aat       734
Gly Lys Leu Ile Pro Glu Leu Asn Asp Arg Leu Lys Ala Val Gln Asn
205                 210                 215                 220

ttc ttt act agc tta tca gtc aca gtg aaa caa gcg aat aaa gat atc       782
Phe Phe Thr Ser Leu Ser Val Thr Val Lys Gln Ala Asn Lys Asp Ile
                225                 230                 235

gat gcg gca aaa ttg aaa tta gcc act gaa ata gca gca att ggg gag       830
Asp Ala Ala Lys Leu Lys Leu Ala Thr Glu Ile Ala Ala Ile Gly Glu
        240                 245                 250
```

```
ata aaa acg gaa acc gaa aca acc aga ttc tac gtt gat tat gat gat        878
Ile Lys Thr Glu Thr Glu Thr Thr Arg Phe Tyr Val Asp Tyr Asp Asp
        255                 260                 265

tta atg ctt tct tta cta aaa gga gct gca aag aaa atg att aac acc        926
Leu Met Leu Ser Leu Leu Lys Gly Ala Ala Lys Lys Met Ile Asn Thr
        270                 275                 280

tgt aat gaa tac caa caa agg cac ggt aag aag acg ctt ctc gag gtt        974
Cys Asn Glu Tyr Gln Gln Arg His Gly Lys Lys Thr Leu Leu Glu Val
285                 290                 295                 300

cct gac atc tga tacattttca ttcgctctgt ttacttttaa cgcccgatag         1026
Pro Asp Ile


cgtgaagaaa atgagagacg gagaaaaagc gatattcaac agcccgataa acaagagtcg      1086

ttaccgggct ggcgag                                                     1102
```

<210> 24
<211> 303
<212> PRT
<213> Salmonella paratyphi

<400> 24

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Met Thr Gly Ile Phe Ala Glu Gln Thr Val Glu Val Val Lys Ser Ala
1               5                   10                  15


Ile Glu Thr Ala Asp Gly Ala Leu Asp Phe Tyr Asn Lys Tyr Leu Asp
            20                  25                  30


Gln Val Ile Pro Trp Lys Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser
        35                  40                  45


Arg Phe Lys Gln Glu Tyr Ser Gln Glu Ala Ser Val Leu Val Gly Asp
    50                  55                  60


Ile Lys Val Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr
65                  70                  75                  80


Gln Thr Val Tyr Glu Trp Cys Gly Val Val Thr Gln Leu Leu Ser Ala
                85                  90                  95


Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Gln
            100                 105                 110
```

Lys Asp Ile Leu Ile Arg Ile Leu Asp Asp Gly Val Asn Lys Leu Asn
        115   120   125

Glu Ala Gln Lys Ser Leu Leu Gly Ser Ser Gln Ser Phe Asn Asn Ala
        130   135   140

Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr Asn Asp Phe Ser
145   150   155   160

Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Arg Ile Arg Lys Glu
                165   170   175

Ala Tyr Ala Gly Ala Ala Ala Gly Ile Val Ala Gly Pro Phe Gly Leu
            180   185   190

Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Ile Glu Gly Lys Leu Ile
        195   200   205

Pro Glu Leu Asn Asp Arg Leu Lys Ala Val Gln Asn Phe Phe Thr Ser
    210   215   220

Leu Ser Val Thr Val Lys Gln Ala Asn Lys Asp Ile Asp Ala Ala Lys
225   230   235   240

Leu Lys Leu Ala Thr Glu Ile Ala Ala Ile Gly Glu Ile Lys Thr Glu
            245   250   255

Thr Glu Thr Thr Arg Phe Tyr Val Asp Tyr Asp Asp Leu Met Leu Ser
            260   265   270

Leu Leu Lys Gly Ala Ala Lys Lys Met Ile Asn Thr Cys Asn Glu Tyr
        275   280   285

Gln Gln Arg His Gly Lys Lys Thr Leu Leu Glu Val Pro Asp Ile
    290   295   300

<210>   25
<211>   904
<212>   DNA
<213>   Shigella flexneri

<220>
<221>   CDS

27/32

<222> (1)..(342)

<400> 25
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atg act gaa atc gtt gca gat aaa acg gta gaa gta gtt aaa aac gca        48
Met Thr Glu Ile Val Ala Asp Lys Thr Val Glu Val Val Lys Asn Ala
1               5                   10                  15

atc gaa acc gca gat gga gca tta gat ctt tat aat aaa tat ctc gat        96
Ile Glu Thr Ala Asp Gly Ala Leu Asp Leu Tyr Asn Lys Tyr Leu Asp
                20                  25                  30

cag gtc atc ccc tgg cag acc ttt gat gaa acc ata aaa gag tta agt       144
Gln Val Ile Pro Trp Gln Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser
            35                  40                  45

cgc ttt aaa cag gag tat tca cag gca gcc tcc gtt tta gtc ggc gat       192
Arg Phe Lys Gln Glu Tyr Ser Gln Ala Ala Ser Val Leu Val Gly Asp
    50                  55                  60

att aaa acc tta ctt atg gat agc cag gat aag tat ttt gaa gca acc       240
Ile Lys Thr Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr
65                  70                  75                  80

caa aca gtg tat gaa tgg tgt ggt gtt gcg acg caa ttg ctc gca gcg       288
Gln Thr Val Tyr Glu Trp Cys Gly Val Ala Thr Gln Leu Leu Ala Ala
                85                  90                  95

tat att ttg cta ttt gat gag tac aat gag aag aaa gca tcc gcc cct       336
Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Pro
            100                 105                 110

cat taa ggtactggat gacggcatca cgaagctgaa tgaagcgcaa aattccctgc        392
His
```

```
tggtaagctc acaaagtttc aacaacgctt ccgggaaact gctggcgtta gatagccagt     452

taaccaatga tttttcagaa aaaagcagct atttccagtc acaggtagat aaaatcagga     512

aggaagcgta tgccggtgcc gcagccggtg tcgtcgccgg tccatttggt ttaatcattt     572

cctattctat tgctgcgggc gtagttgaag ggaaactgat tccagaattg aagaacaagt     632

taaaatctgt gcagagtttc tttaccaccc tgtctaacac ggttaaacaa gcgaataaag     ·692

atatcgatgc cgccaaattg aaattaacca ccgaaatagc cgccatcggg gagataaaaa     752

cggaaactga aaccaccaga ttctatgttg attatgatga tttaatgctt tctttgctaa     812

aagcagcggc caaaaaaatg attaacacct gtaatgagta tcagaaaaga cacggtaaaa     872

agacactctt tgaggtacct gaagtctgat aa                                   904
```

<210> 26
<211> 113

```
<212>   PRT
<213>   Shigella flexneri

<400>   26

Met Thr Glu Ile Val Ala Asp Lys Thr Val Glu Val Val Lys Asn Ala
1               5                   10                  15


Ile Glu Thr Ala Asp Gly Ala Leu Asp Leu Tyr Asn Lys Tyr Leu Asp
            20                  25                  30


Gln Val Ile Pro Trp Gln Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser
            35                  40                  45


Arg Phe Lys Gln Glu Tyr Ser Gln Ala Ala Ser Val Leu Val Gly Asp
        50                  55                  60


Ile Lys Thr Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr
65                  70                  75                  80


Gln Thr Val Tyr Glu Trp Cys Gly Val Ala Thr Gln Leu Leu Ala Ala
                85                  90                  95


Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Pro
            100                 105                 110


His


<210>   27
<211>   1080
<212>   DNA
<213>   Escherichia coli


<220>
<221>   CDS
<222>   (121)..(1032)

<400>   27
agaaataaag acattgacgc atcccgcccg gctaactatg aattagatga agtaaaattt       60

attaatagtt gtaaaacagg agtttcatta caatttatat atttaaagag gcgaatgatt      120

atg act gaa atc gtt gca gat aaa acg gta gaa gta gtt aaa aac gca       168
Met Thr Glu Ile Val Ala Asp Lys Thr Val Glu Val Val Lys Asn Ala
1               5                   10                  15
```

29/32

```
atc gaa acc gca gat gga gca tta gat ctt tat aat aaa tat ctc gat          216
Ile Glu Thr Ala Asp Gly Ala Leu Asp Leu Tyr Asn Lys Tyr Leu Asp
            20                  25              30

cag gtc atc ccc tgg cag acc ttt gat gaa acc ata aaa gag tta agt          264
Gln Val Ile Pro Trp Gln Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser
            35                  40              45

cgc ttt aaa cag gag tat tca cag gca gcc tcc gtt tta gtc ggc gat          312
Arg Phe Lys Gln Glu Tyr Ser Gln Ala Ala Ser Val Leu Val Gly Asp
            50                  55              60

att aaa acc tta ctt atg gat agc cag gat aag tat ttt gaa gca acc          360
Ile Lys Thr Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr
65                  70                  75                  80

caa aca gtg tat gaa tgg tgt ggt gtt gcg acg caa ttg ctc gca gcg          408
Gln Thr Val Tyr Glu Trp Cys Gly Val Ala Thr Gln Leu Leu Ala Ala
                    85                  90                  95

tat att ttg cta ttt gat gag tac aat gag aag aaa gca tcc gcc cag          456
Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Gln
                100                 105                 110

aaa gac att ctc att aag gta ctg gat gac ggc atc acg aag ctg aat          504
Lys Asp Ile Leu Ile Lys Val Leu Asp Asp Gly Ile Thr Lys Leu Asn
            115                 120                 125

gaa gcg caa aaa tcc ctg ctg gta agc tca caa agt ttc aac aac gct          552
Glu Ala Gln Lys Ser Leu Leu Val Ser Ser Gln Ser Phe Asn Asn Ala
            130                 135                 140

tcc ggg aaa ctg ctg gcg tta gat agc cag tta acc aat gat ttt tca          600
Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr Asn Asp Phe Ser
145                 150                 155                 160

gaa aaa agc agc tat ttc cag tca cag gta gat aaa atc agg aag gaa          648
Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Lys Ile Arg Lys Glu
                165                 170                 175

gca tat gcc ggt gcc gca gcc ggt gtc gtc gcc ggt cca ttt gga tta          696
Ala Tyr Ala Gly Ala Ala Ala Gly Val Val Ala Gly Pro Phe Gly Leu
                180                 185                 190

atc att tcc tat tct att gct gcg ggc gta gtt gaa gga aaa ctg att          744
Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Val Glu Gly Lys Leu Ile
            195                 200                 205

cca gaa ttg aag aac aag tta aaa tct gtg cag aat ttc ttt acc acc          792
Pro Glu Leu Lys Asn Lys Leu Lys Ser Val Gln Asn Phe Phe Thr Thr
            210                 215                 220

ctg tct aac acg gtt aaa caa gcg aat aaa gat atc gat gcc gcc aaa          840
Leu Ser Asn Thr Val Lys Gln Ala Asn Lys Asp Ile Asp Ala Ala Lys
225                 230                 235                 240
```

```
ttg aaa tta acc acc gaa ata gcc gcc atc ggt gag ata aaa acg gaa      888
Leu Lys Leu Thr Thr Glu Ile Ala Ala Ile Gly Glu Ile Lys Thr Glu
            245                 250                 255

act gaa aca acc aga ttc tac gtt gat tat gat gat tta atg ctt tct      936
Thr Glu Thr Thr Arg Phe Tyr Val Asp Tyr Asp Asp Leu Met Leu Ser
            260                 265                 270

ttg cta aaa gaa gcg gcc aaa aaa atg att aac acc tgt aat gag tat      984
Leu Leu Lys Glu Ala Ala Lys Lys Met Ile Asn Thr Cys Asn Glu Tyr
            275                 280                 285

cag aaa aga cac ggt aaa aag aca ctc ttt gag gta cct gaa gtc tga     1032
Gln Lys Arg His Gly Lys Lys Thr Leu Phe Glu Val Pro Glu Val
        290                 295                 300

taagcgatta ttctctccat gtactcaagg tataaggttt atcacatt              1080


<210>  28
<211>  303
<212>  PRT
<213>  Escherichia coli

<400>  28

Met Thr Glu Ile Val Ala Asp Lys Thr Val Glu Val Val Lys Asn Ala
1               5                   10                  15


Ile Glu Thr Ala Asp Gly Ala Leu Asp Leu Tyr Asn Lys Tyr Leu Asp
            20                  25                  30


Gln Val Ile Pro Trp Gln Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser
        35                  40                  45


Arg Phe Lys Gln Glu Tyr Ser Gln Ala Ala Ser Val Leu Val Gly Asp
    50                  55                  60


Ile Lys Thr Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr
65                  70                  75                  80


Gln Thr Val Tyr Glu Trp Cys Gly Val Ala Thr Gln Leu Leu Ala Ala
                85                  90                  95


Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Gln
            100                 105                 110


Lys Asp Ile Leu Ile Lys Val Leu Asp Asp Gly Ile Thr Lys Leu Asn
        115                 120                 125
```

31/32

```
Glu Ala Gln Lys Ser Leu Leu Val Ser Ser Gln Ser Phe Asn Asn Ala
    130             135             140


Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr Asn Asp Phe Ser
145             150             155             160


Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Lys Ile Arg Lys Glu
                165             170             175


Ala Tyr Ala Gly Ala Ala Ala Gly Val Val Ala Gly Pro Phe Gly Leu
                180             185             190


Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Val Glu Gly Lys Leu Ile
    .195             200             205


Pro Glu Leu Lys Asn Lys Leu Lys Ser Val Gln Asn Phe Phe Thr Thr
    210             215             220


Leu Ser Asn Thr Val Lys Gln Ala Asn Lys Asp Ile Asp Ala Ala Lys
225             230             235             240


Leu Lys Leu Thr Thr Glu Ile Ala Ala Ile Gly Glu Ile Lys Thr Glu
                245             250             255


Thr Glu Thr Thr Arg Phe Tyr Val Asp Tyr Asp Asp Leu Met Leu Ser
                260             265             270


Leu Leu Lys Glu Ala Ala Lys Lys Met Ile Asn Thr Cys Asn Glu Tyr
    275             280             285


Gln Lys Arg His Gly Lys Lys Thr Leu Phe Glu Val Pro Glu Val
    290             295             300
```